



N 0400  
5-2-01.

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/829,066  
Source: OIPF  
Date Processed by STIC: 4/30/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION
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SERIAL NUMBER: 09/829,066

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- |          |                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|----------|---------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 _____  | Wrapped Nucleics                | The number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".                                                                                                                                                                                                                          |
| 2 _____  | Wrapped Aminos                  | The amino acid number/text at the end of each line "wrapped " down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".                                                                                                                                                                                                              |
| 3 _____  | Incorrect Line Length           | The rules require that a line not exceed 72 characters in length. This includes spaces.                                                                                                                                                                                                                                                                                                                                                                          |
| 4 _____  | Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.                                                                                                                                                                                                                                                                    |
| 5 _____  | Non-ASCII                       | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.<br>Please ensure your subsequent submission is saved in ASCII text so that it can be processed.                                                                                                                                                                                                                                                                                  |
| 6 _____  | Variable Length                 | Sequence(s) _____ contain n's or Xaa's which represented more than one residue.<br>As per the rules, each n or Xaa can only represent a single residue.<br>Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.                                                                                                                                                           |
| 7 _____  | PatentIn ver. 2.0 "bug"         | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies primarily to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>              |
| 8 _____  | Skipped Sequences (OLD RULES)   | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:<br><b>(2) INFORMATION FOR SEQ ID NO:X:</b><br><b>(i) SEQUENCE CHARACTERISTICS:</b> (Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br><b>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:</b><br><b>This sequence is intentionally skipped</b><br><br>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 _____  | Skipped Sequences (NEW RULES)   | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.<br><b>&lt;210&gt; sequence id number</b><br><b>&lt;400&gt; sequence id number</b><br><b>000</b>                                                                                                                                                                                                                                                            |
| 10 _____ | Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.                                                                                                                                                                                                                 |
| 11 _____ | Use of "Artificial" (NEW RULES) | Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.<br>Valid response is Artificial Sequence.                                                                                                                                                                                                                                                                                                               |
| 12 _____ | Use of <220>Feature (NEW RULES) | Sequence(s) _____ are missing the <220>Feature and associated headings.<br>Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"<br>Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)                                                                                                                      |
| 13 _____ | PatentIn ver. 2.0 "bug"         | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.                                                                                                                                                                     |

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt

Output Set: N:\CRF3\04302001\I829066.raw

Does Not Comply  
Corrected Diskette Needed

pg 1-3

4 <110> APPLICANT: Nisson, Paul  
 5 Jesse, Joel  
 6 Li, Wu-bo  
 8 <120> TITLE OF INVENTION: Method for Isolating and Recovering Target DNA or RNA  
 Molecules Having  
 9 a Desired Nucleotide Sequence  
 11 <130> FILE REFERENCE: 0942.4800002  
 W--> 14 <140> CURRENT APPLICATION NUMBER: US/09/829,066  
 14 <141> CURRENT FILING DATE: 2001-04-10  
 16 <150> PRIOR APPLICATION NUMBER: US 09/103,577  
 17 <151> PRIOR FILING DATE: 1998-06-24  
 19 <160> NUMBER OF SEQ ID NOS: 11  
 21 <170> SOFTWARE: PatentIn version 3.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 23  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Oligonucleotide/Primer  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: misc\_feature  
 32 <222> LOCATION: 3  
 33 <223> OTHER INFORMATION: N is G, T, A, or C  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: misc\_feature  
 37 <222> LOCATION: 6  
 38 <223> OTHER INFORMATION: Y is C or T  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: misc\_feature  
 42 <222> LOCATION: 9  
 43 <223> OTHER INFORMATION: Y is C or T  
 45 <220> FEATURE:  
 46 <221> NAME/KEY: misc\_feature  
 47 <222> LOCATION: 12  
 48 <223> OTHER INFORMATION: N is G, T, A, or C  
 50 <220> FEATURE:  
 51 <221> NAME/KEY: misc\_feature  
 52 <222> LOCATION: 15  
 53 <223> OTHER INFORMATION: Y is C or T  
 55 <220> FEATURE:  
 56 <221> NAME/KEY: misc\_feature  
 57 <222> LOCATION: 18  
 58 <223> OTHER INFORMATION: Y is C or T  
 60 <220> FEATURE:  
 61 <221> NAME/KEY: misc\_feature  
 62 <222> LOCATION: 21  
 63 <223> OTHER INFORMATION: N is G, T, A, or C  
 66 <400> SEQUENCE: 1  
 W--> 67 gtntgygag gnttycaygt ngg  
 71 <210> SEQ ID NO: 2

(global error)  
 invalid - Per 1.823 of sequence rules, the only valid  
 <213> responses are: Unknown,  
 Artificial Sequence, or  
 Scientific name  
 (Genus/species)  
 (one of the three)  
 see circled portion  
 of Item 12 on Error  
 Summary Sheet

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt

Output Set: N:\CRF3\04302001\I829066.raw

72 <211> LENGTH: 19	
73 <212> TYPE: DNA	
74 <213> ORGANISM: Oligonucleotide/Primer	
77 <400> SEQUENCE: 2	
78 gtkttggaggk ttcagtkgg	19
82 <210> SEQ ID NO: 3	
83 <211> LENGTH: 18	
84 <212> TYPE: DNA	
85 <213> ORGANISM: Oligonucleotide/Primer	
88 <400> SEQUENCE: 3	
89 gtkttggaggk ttcagtg	18
93 <210> SEQ ID NO: 4	
94 <211> LENGTH: 18	
95 <212> TYPE: DNA	
96 <213> ORGANISM: Oligonucleotide/Primer	
99 <400> SEQUENCE: 4	
100 gtkttggagggt tcagtkgg	18
104 <210> SEQ ID NO: 5	
105 <211> LENGTH: 18	
106 <212> TYPE: DNA	
107 <213> ORGANISM: Oligonucleotide/Primer	
111 <400> SEQUENCE: 5	
112 gttggagggt tcagtkgg	18
116 <210> SEQ ID NO: 6	
117 <211> LENGTH: 17	
118 <212> TYPE: DNA	
119 <213> ORGANISM: Oligonucleotide/Primer	
123 <400> SEQUENCE: 6	
124 gttggagggt tcagtg	17
128 <210> SEQ ID NO: 7	
129 <211> LENGTH: 17	
130 <212> TYPE: DNA	
131 <213> ORGANISM: Oligonucleotide/Primer	
135 <400> SEQUENCE: 7	
136 gtkttggagggt tcagtg	17
140 <210> SEQ ID NO: 8	
141 <211> LENGTH: 17	
142 <212> TYPE: DNA	
143 <213> ORGANISM: Oligonucleotide/Primer	
147 <400> SEQUENCE: 8	
148 gttggagggt cagtkgg	17
152 <210> SEQ ID NO: 9	
153 <211> LENGTH: 16	
154 <212> TYPE: DNA	
155 <213> ORGANISM: Oligonucleotide/Primer	
157 <400> SEQUENCE: 9	
158 gttggagggt cagtg	16
162 <210> SEQ ID NO: 10	
163 <211> LENGTH: 25	

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt

Output Set: N:\CRF3\04302001\I829066.raw

164 <212> TYPE: DNA  
165 <213> ORGANISM: Oligonucleotide/Primer  
167 <400> SEQUENCE: 10  
168 gaccgttcag ctggatatta cggcc  
172 <210> SEQ ID NO: 11  
173 <211> LENGTH: 13  
174 <212> TYPE: DNA  
175 <213> ORGANISM: Oligonucleotide/Primer  
176 <223> OTHER INFORMATION: consensus sequence for initiation of translation  
179 <400> SEQUENCE: 11  
180 gccgccagcc aug

25

13

insert this  
mandatory  
numeric  
identifier  
whenever  
C2217, C2227,  
or C2237 is  
shown.  
C2207 never  
has a response;  
it is a "header"  
only.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:25

Input Set : A:\seqlist-09424800001.txt

Output Set: N:\CRF3\04302001\I829066.raw

L:14 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.

L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1